

FIGURE 1A.1



APPROVED	O.G. FIC.
BY	CLASS. SUBCLASS
DRAFTSMAN	

ATG AAG CCG TAC TTC TGC CGT GTC TTT GTC TTC TGC TTC CTA ATC	45
M K P Y F C R V F V F C F L I	
5 10 15	
AGA CTT TTA ACA GGA GAA ATC AAT GGC TCG GCC GAT CAT AGG ATG	90
R L L T G *E I N G S A D H R M	
20 25 30	
TTT TCA TTT CAC AAT GGA GGT GTA CAG ATT TCT TGT AAA TAC CCT	135
F S F H N G G V Q I S C K Y P	
35 40 45	
GAG ACT GTC CAG CAG TTA AAA ATG CGA TTG TTC AGA GAG AGA GAA	180
E T V Q Q L K M R L F R E R E	
50 55 60	
GTC CTC TGC GAA CTC ACC AAG ACC AAG GGA AGC GGA AAT GCG GTG	225
V L C E L T K T K G S G N A V	
65 70 75	
TCC ATC AAG AAT CCA ATG CTC TGT CTA TAT CAT CTG TCA AAC AAC	270
S I K N P M L C L Y H L S N N	
80 85 90	
AGC GTC TCT TTT TTC CTA AAC AAC CCA GAC AGC TCC CAG GGA AGC	315
S V S F F L N N P D S S Q G S	
95 100 105	
TAT TAC TTC TGC AGC CTG TCC ATT TTT GAC CCA CCT CCT TTT CAA	360
Y Y F C S L S I F D P P P F Q	
110 115 120	
GAA AGG AAC CTT AGT GGA GGA TAT TTG CAT ATT TAT GAA TCC CAG	405
E R N L S G G Y L H I Y E S Q	
125 130 135	
CTC TGC TGC CAG CTG AAG CTC TGG CTA CCC GTA GGG TGT GCA GCT	450
L C C Q L K L W L P V G C A A	
140 145 150	
TTC GTT GTG GTA CTC CTT TTT GGA TGC ATA CTT ATC ATC TGG TTT	495
F V V V L L F G C I L I I W F	
155 160 165	
TCA AAA AAG AAA TAC GGA TCC AGT GTG CAT GAC CCT AAT AGT GAA	540
S K K K Y G S S V H D P N S E	
170 175 180	



FIGURE 1A.2

APPROVED	O.G. FIG.
BY	CLASS. SUBCLASS
DRAFTSMAN	

TAC	ATG	TTC	ATG	GCG	GCA	GTC	AAC	ACA	AAC	AAA	AAG	TCT	AGA	CTT	585
Y	M	F	M	A	A	V	N	T	N	K	K	S	R	L	
				185					190					195	
GCA GGT GTG ACC TCA															600
A	G	V	T	S											
				200											

FIGURE 1B



APPROVED	CLASS	FIG.
BY	SUBCLASS	
DRAFTSMAN		

mCRP1	MKPYFCRVFV	FCFLIRLL--	-----TGEIN	GS----	ADHR	MFSFHNGGVQ	39
mCD28	MT-----	----LRLLFL	ALNFFSVQVT	ENKILVKQSP	LLVVDSENEVS		38
Consensus	M.....RLL..V.		
mCRP1	ISCKYPETV-	-QQLKMRLFR	--EREV-LCE	LTKTKGSGNA	VSIKNPMLCL		84
mCD28	LSCRYSYNLL	AKEFRASLYK	GVNSDVEVCV	GNGNFTYQPQ	FRSNAEFNCD		88
Consensus	.SC.Y.....L..V..C.C.		
mCRP1	YHLSNNSVSF	FLNPNDSQOG	SYFCSLSIF	DPPPFQERNL	SGGYL-HIYE		133
mCD28	GDFDNETVTF	RLWNLHVNHT	DIYFCKIEFM	YPPPYLDNER	SNGTIIHIKE		138
ConsensusN..V.F	.L.N.....	..YFC.....	.PPP.....	S.G...HI.E		
mCRP1	SQLC---CQL	KL-W-LPVGC	AA-FVVLLF	GCIL-IIWFS	KKKY----GS		172
mCD28	KHLCHTQSSP	KLFWALVVVA	GVLFCYGLLV	TVALCVIWTN	SRRNRLQVT		188
Consensus	..LC.....	KL.W.L.V..	...F...LL.	...L..IW..		
mCRP1	SVH-DPNSEY	MFMAAVNTNK	KSR-LAGVTS				200
mCD28	TMNMTPRRPG	LTRKPYQPYA	PARDFAAYRP				218
ConsensusP.....R..A....			



FIGURE 2A.1

ATG CAG CTA AAG TGT CCC TGT TTT GTG TCC TTG GGA ACC AGG CAG	45
M Q L K C P C F V S L G T R Q	
5 10 15	
CCT GTT TGG AAG AAG CTC CAT GTT TCT AGC GGG TTC TTT TCT GGT	90
P V W K K L H V S S G F F S G	
20 25 30	
CTT GGT CTG TTC TTG CTG CTG TTG AGC AGC CTC TGT GCT GCC TCT	135
L G L F L L L L S S L C A A S	
35 40 45	
GCA GAG ACT GAA GTC GGT GCA ATG GTG GGC AGC AAT GTG GTG CTC	180
A *E T E V G A M V G S N V V L	
50 55 60	
AGC TGC ATT GAC CCC CAC AGA CGC CAT TTC AAC TTG AGT GGT CTG	225
S C I D P H R R H F N L S G L	
65 70 75	
TAT GTC TAT TGG CAA ATC GAA AAC CCA GAA GTT TCG GTG ACT TAC	270
Y V Y W Q I E N P E V S V T Y	
80 85 90	
TAC CTG CCT TAC AAG TCT CCA GGG ATC AAT GTG GAC AGT TCC TAC	315
Y L P Y K S P G I N V D S S Y	
95 100 105	
AAG AAC AGG GGC CAT CTG TCC CTG GAC TCC ATG AAG CAG GGT AAC	360
K N R G H L S L D S M K Q G N	
110 115 120	
TTC TCT CTG TAC CTG AAG AAT GTC ACC CCT CAG GAT ACC CAG GAG	405
F S L Y L K N V T P Q D T Q E	
125 130 135	
TTC ACA TGC CGG GTA TTT ATG AAT ACA GCC ACA GAG TTA GTC AAG	450
F T C R V F M N T A T E L V K	
140 145 150	
ATC TTG GAA GAG GTG GTC AGG CTG CGT GTG GCA GCA AAC TTC AGT	495
I L E E V V R L R V A A N F S	
155 160 165	
ACA CCT GTC ATC AGC ACC TCT GAT AGC TCC AAC CCG GGC CAG GAA	540
T P V I S T S D S S N P G Q E	
170 175 180	

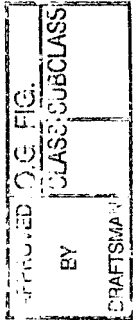
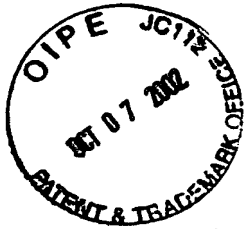


FIGURE 2A.2

CGT ACC TAC ACC TGC ATG TCC AAG AAT GGC TAC CCA GAG CCC AAC	585
R T Y T C M S K N G Y P E P N	
185 190 195	
CTG TAT TGG ATC AAC ACA ACG GAC AAT AGC CTA ATA GAC ACG GCT	630
L Y W I N T T D N S L I D T A	
200 205 210	
CTG CAG AAT AAC ACT GTC TAC TTG AAC AAG TTG GGC CTG TAT GAT	675
L Q N N T V Y L N K L G L Y D	
215 220 225	
GTA ATC AGC ACA TTA AGG CTC CCT TGG ACA TCT CGT GGG GAT GTT	720
V I S T L R L P W T S R G D V	
230 235 240	
CTG TGC TGC GTA GAG AAT GTG GCT CTC CAC CAG AAC ATC ACT AGC	765
L C C V E N V A L H Q N I T S	
245 250 255	
ATT AGC CAG GCA GAA AGT TTC ACT GGA AAT AAC ACA AAG AAC CCA	810
I S Q A E S F T G N N T K N P	
260 265 270	
CAG GAA ACC CAC AAT AAT GAG TTA AAA GTC CTT GTC CCC GTC CTT	855
Q E T H N N E L K V L V P V L	
275 280 285	
GCT GTA CTG GCG GCA GCG GCA TTC GTT TCC TTC ATC ATA TAC AGA	900
A V L A A A A F V S F I I Y R	
290 295 300	
CGC ACG CGT CCC CAC CGA AGC TAT ACA GGA CCC AAG ACT GTA CAG	945
R T R P H R S Y T G P K T V Q	
305 310 315	
CTT GAA CTT ACA GAC CAC GCC	966
L E L T D H A	
320 322	

FIG. 1

EV

DRAFTSMAN

CLASS

mB7RP1	MQLKPCPCFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLS-	SLCAASAETE	49
mCD80	MA--CNC--Q	LMQDTPL---	LKFPCPRI-	L-LFVLLIRL	SQVSSDVDEQ	41
Consensus	M...C.C...	L....P....	L.....	L.LF.LL...	S.....	
mB7RP1	VGAMVGSNVV	LSCIDPHRRH	FNLSGLYVYW	QIENPEVSVT	YYLPYKSPGI	99
mCD80	LSKSVKDKVL	LPC-RYNSPH	EDESEDRIYW	QKHKDVV---	--LSVIAGKL	85
ConsensusV...V.	L.C.....H	...S....YW	Q.....V...	..L.....	
mB7RP1	NVDSSYKNRG	HLSLDSMKQG	NFSLYLKNVT	PQDTQEFTCR	VFMNTATELV	149
mCD80	KVWPEYKNR-	--TL--YDNT	TYSLIILGLV	LSDRGTYSKV	VQKKERGTYE	130
Consensus	.V...YKNR.	...L.....	..SL.....	..D.....C.	V.....	
mB7RP1	KILEEVVRLR	VAANFSTPVI	STSDSSNPGQ	ERTYTCMSKN	GYPEPNLYWI	199
mCD80	VKHLALVKLS	IKADFSTPNI	TESGNPSADT	KRI-TCFASG	GFPKPRFSWL	179
ConsensusV.L.	..A.FSTP.I	..S.....	.R..TC....	G.P.P...W.	
mB7RP1	-NTTDSLID	TALQNNTVYL	NKLGLYDVIS	TLRLPWTSRG	DVLCCVENVA	248
mCD80	ENGRELPGIN	TTISQDPESE	LYTISSQLDF	NTRNHTIKC	LIKYGDAHVS	229
Consensus	.N.....I.	T.....T...V.	
mB7RP1	LHQNITSISQ	AESFTGNNTK	NPQETHNNEL	KVLVPVLAVL	A-AAAFVSFI	297
mCD80	EDFTWEKPPE	DPPDSKNTLV	LFGAGFGAVI	TVVVIVVVIK	CFCKHRSCFR	279
ConsensusN...V.V.V....F.	
mB7RP1	IYRRTR-PHR	SYT-GPKTVQ	LELTDHA			322
mCD80	RNEASRETNN	SLTFGPPEAL	AEQTVFL			306
ConsensusR....	S.T.GP....	.E.T...			



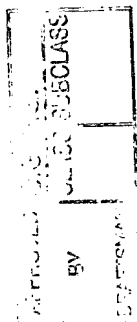
FIGURE 3A.1

ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC	45
M R L G S P G L L F L L F S S	
5 10 15	
CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC	90
L R A *D *T *Q *E K *E V R A *M V G	
20 25 30	
AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT	135
S D V E L S C A C P E G S R F	
35 40 45	
GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA	180
D L N D V Y V Y W Q T S E S K	
50 55 60	
ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC	225
T V V T Y H I P Q N S S L E N	
65 70 75	
GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC	270
V D S R Y R N R A L M S P A G	
80 85 90	
ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC	315
M L R G D F S L R L F N V T P	
95 100 105	
CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG	360
Q D E Q K F H C L V L S Q S L	
110 115 120	
GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA	405
G F Q E V L S V E V T L H V A	
125 130 135	
GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC	450
A N F S V P V V S A P H S P S	
140 145 150	
CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC	495
Q D E L T F T C T S I N G Y P	
155 160 165	
AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG	540
R P N V Y W I N K T D N S L L	
170 175 180	

FIG. 3A.1
CLASS. 360
BY
DRAFTS/JA



FIGURE 3A.2



GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC	585
D Q A L Q N D T V F L N M R G	
185 190 195	
TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC	630
L Y D V V S V L R I A R T P S	
200 205 210	
GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC	675
V N I G C C I E N V L L Q Q N	
215 220 225	
CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC	720
L T V G S Q T G N D I G E R D	
230 235 240	
AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC	765
K I T E N P V S T G E K N A A	
245 250 255	
ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG	810
T W S I L A V L C L L V V V A	
260 265 270	
GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC	855
V A I G W V C R D R C L Q H S	
275 280 285	
TAT GCA GGT	864
Y A G	
288	

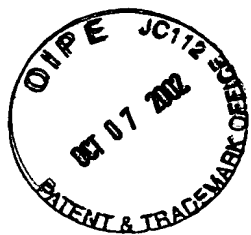
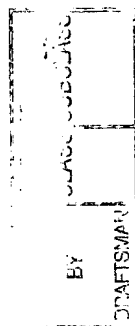


FIGURE 3B



hB7RP1	EKEVRAMVGS	DVELSCACPE	GSRFDLNDVY	VYWQTSESKT	VVTYHIPQNS	50
mB7RP1	ETEVGAMVGS	NVVLSCIDPH	RRHFNLSGLY	VYWQIENPEV	SVTYLPPYKS	50
Consensus	E.EV.AMVGS	.V.LSC..P.	...F.L...Y	VYWQ.....	.VTY..P..S	
hB7RP1	SLENVDSRYR	NRALMSPAGM	LRGDFSLRLF	NVTPQDEQKF	HCLVLSQ-SL	99
mB7RP1	PGINVDSSYK	NRGHLSDLDSM	KQGNFSLYLK	NVTPQDTQEF	TCRVFMNTAT	100
Consensus	...NVDS.Y.	NR...S...M	..G.FSL.L.	NVTPQD.Q.F	.C.V.....	
hB7RP1	GFQEVLSVEV	TLHVAANFSV	PVVSAPHSPS	Q-DELTFTCT	SINGYPRPNV	148
mB7RP1	ELVKILEEVV	RLRVAANFST	PVISTSDSSN	PGQERTYTCM	SKNGYPEPNL	150
ConsensusL...V	.L.VAANFS.	PV.S...S..	...E.T.TC.	S.NGY.P.N.	
hB7RP1	YWINKTDNSL	LDQALQNDTV	FLNMRGLYDV	VSVLRIARTP	SVNIGCCIE	198
mB7RP1	YWINTTDNSL	IDTALQNTTV	YLNKLGlyDV	ISTLRLPWTS	RGDVLCCVEN	200
Consensus	YWIN.TDNSL	.D.ALQN.TV	.LN..GLYDV	.S.LR...T.CC.EN	
hB7RP1	VLLQQNLTVG	SQTGNDIGER	DKITENPVST	GEKNAATWSI	LAVLCLLVVV	248
mB7RP1	VALHQNITSI	SQAESFTGNN	TKNPQETHNN	ELKVLV--PV	LAVLAAAFV	248
Consensus	V.L.QN.T..	SQ.....G..	.K.....	..K.....	LAVL.....V	
hB7RP1	AVAIGWVCRD	RCLQHSYAG				267
mB7RP1	SFIIYR--RT	R-PHRSYTG	KTVQLELTDH	A		276
Consensus	...I....R.	R....SY.G.			

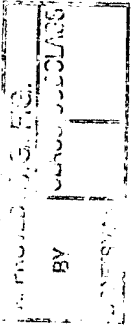
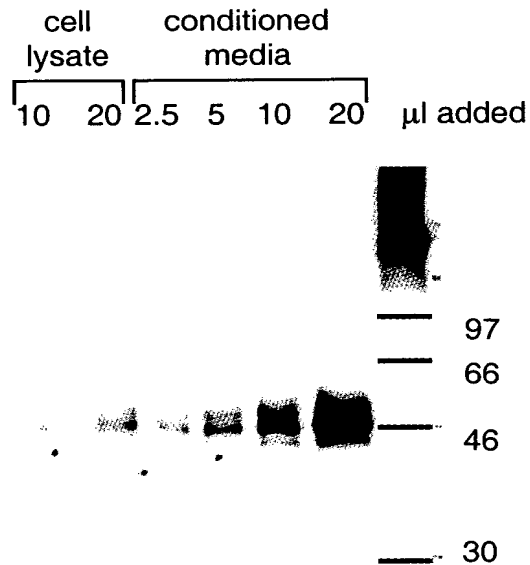


FIG. 4A



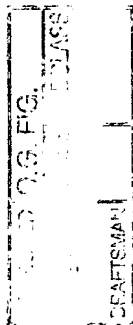
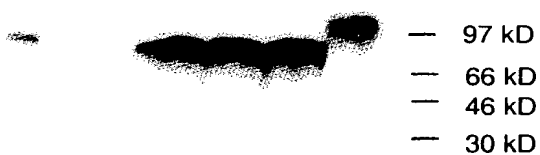
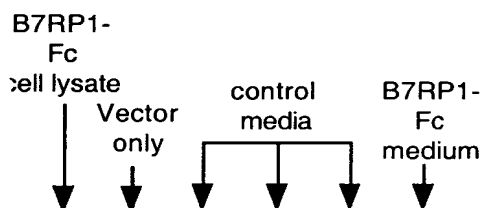


FIG. 4B

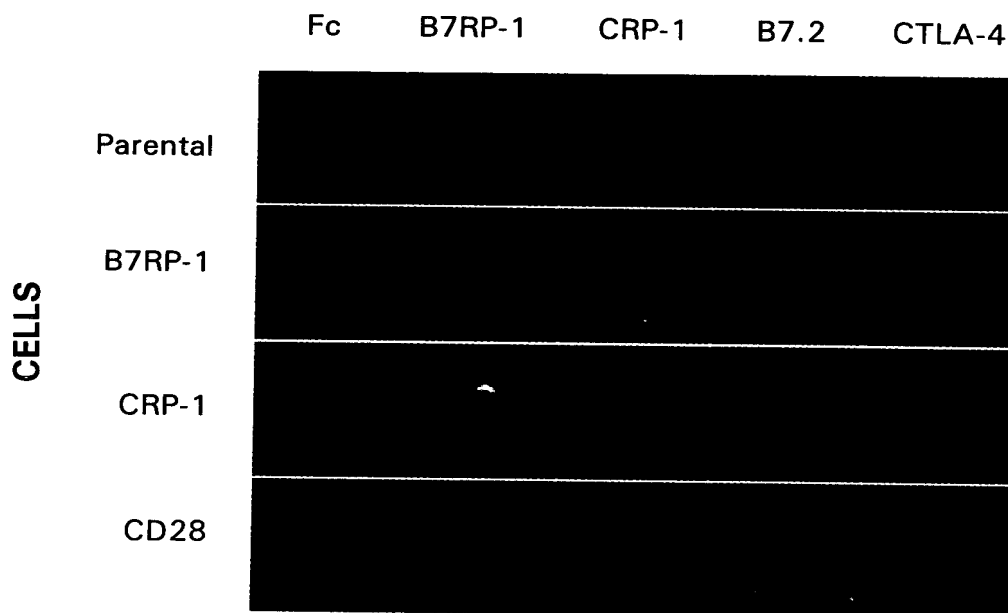




CLASS	SUBCLASS
BY	DRAFTSMAN

FIG. 5

FC FUSION PROTEINS



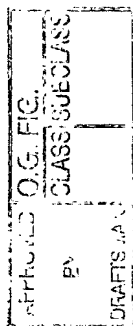


FIG. 6A

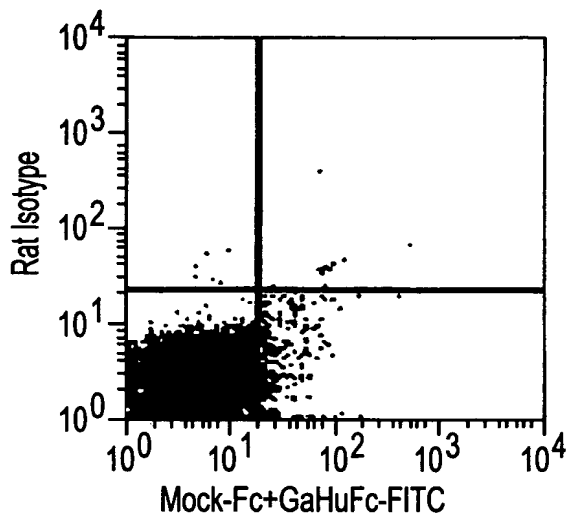


FIG. 6B

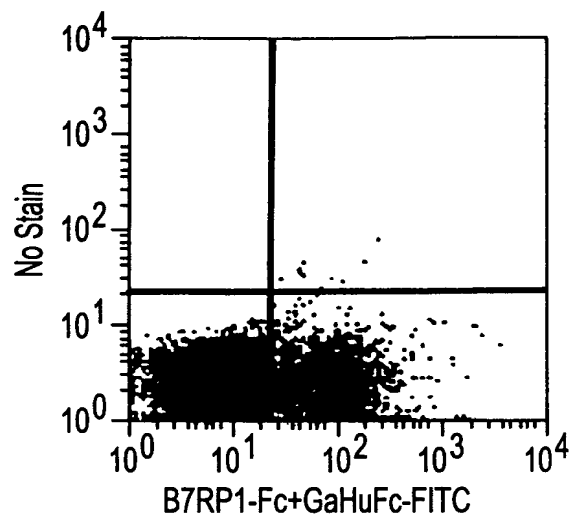


FIG. 6C

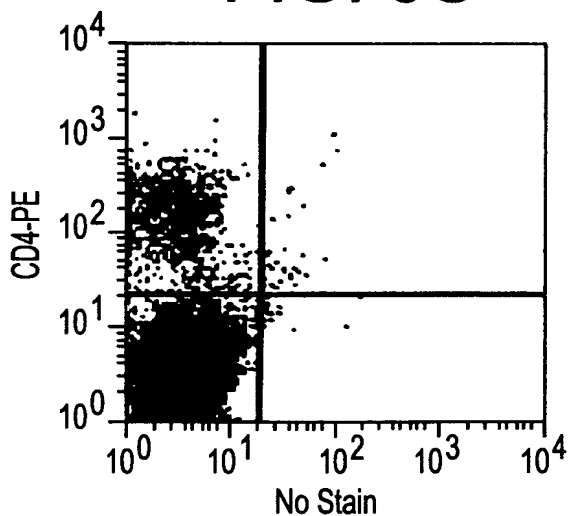


FIG. 6D

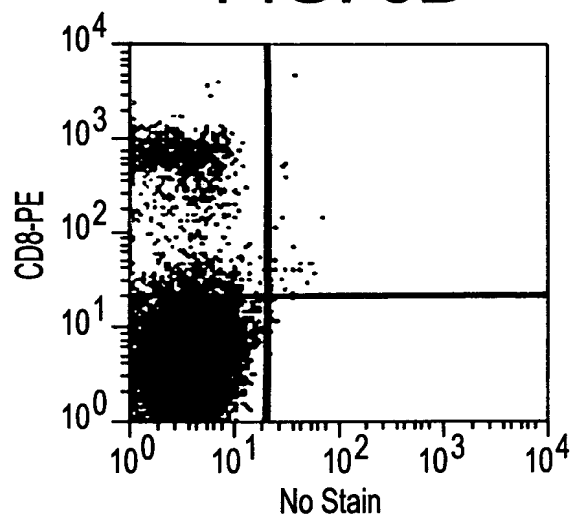


FIG. 6E

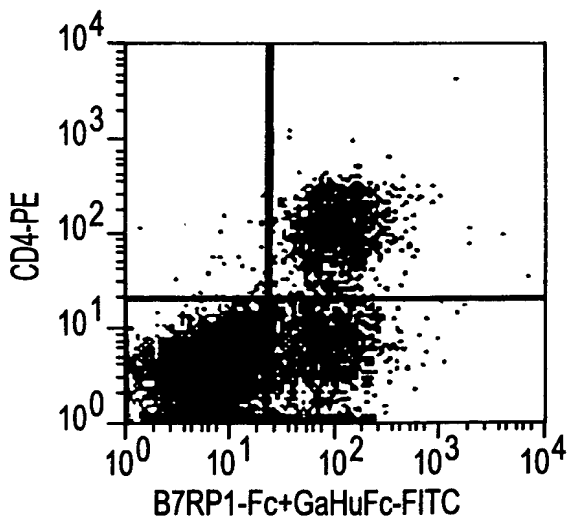


FIG. 6F

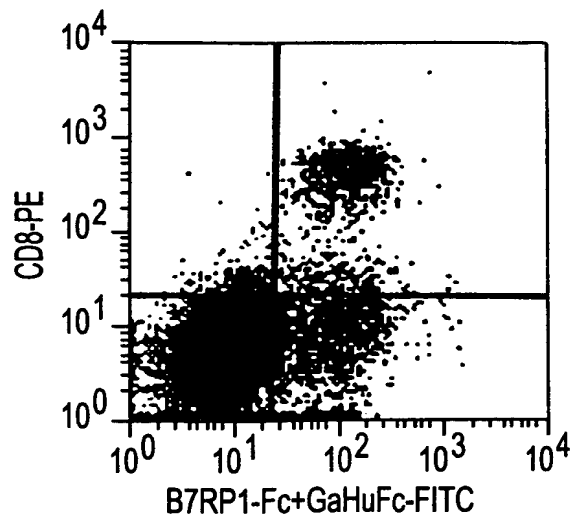




FIG. 7A

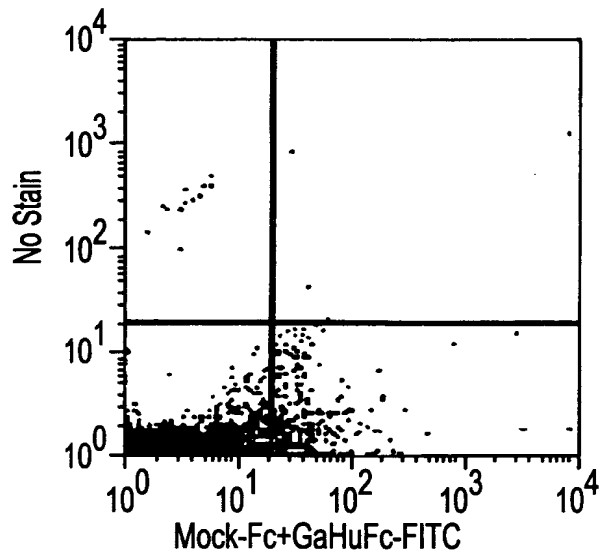


FIG. 7B

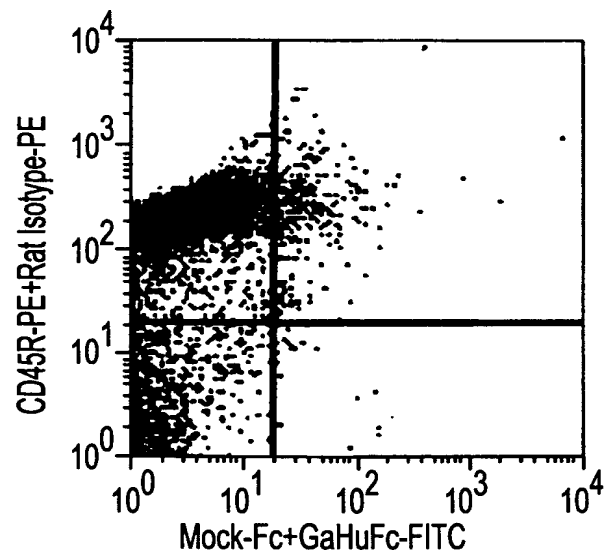


FIG. 7C

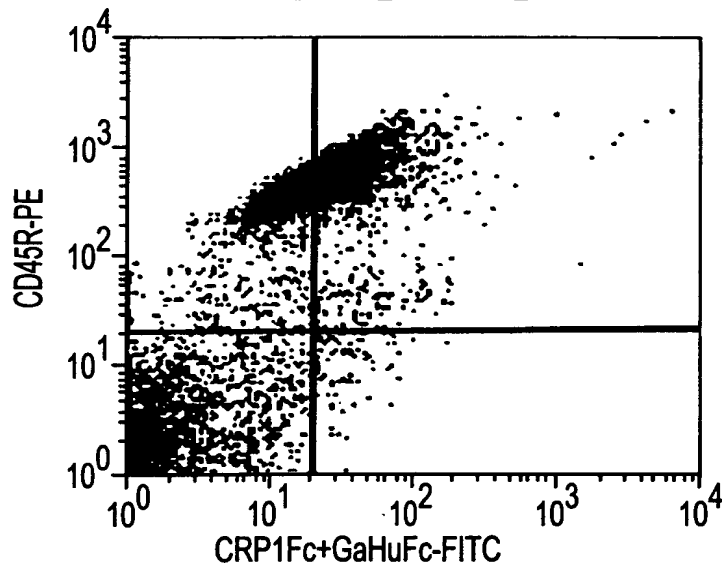




FIG. 8A

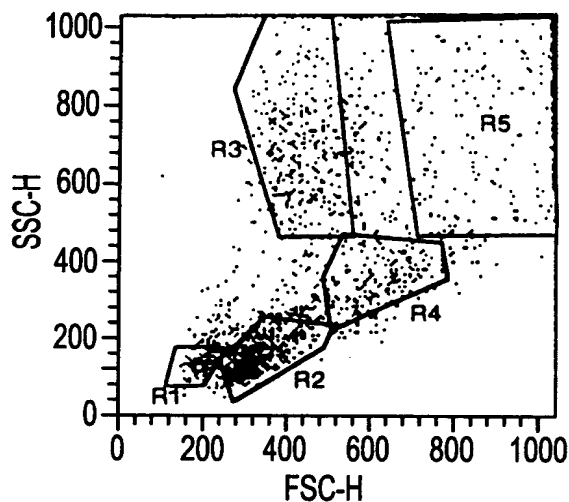


FIG. 8B

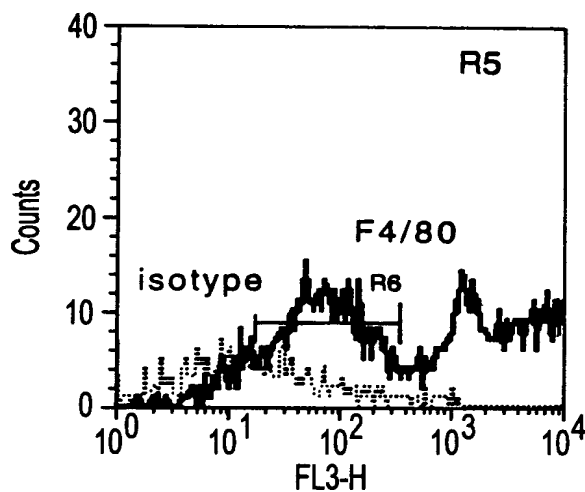
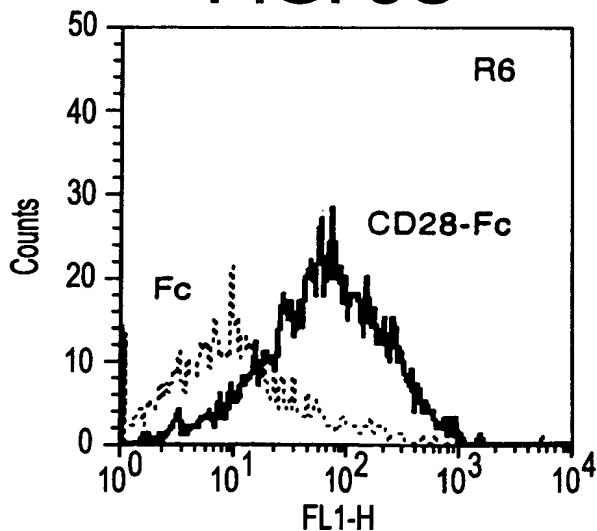


FIG. 8C



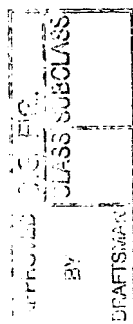
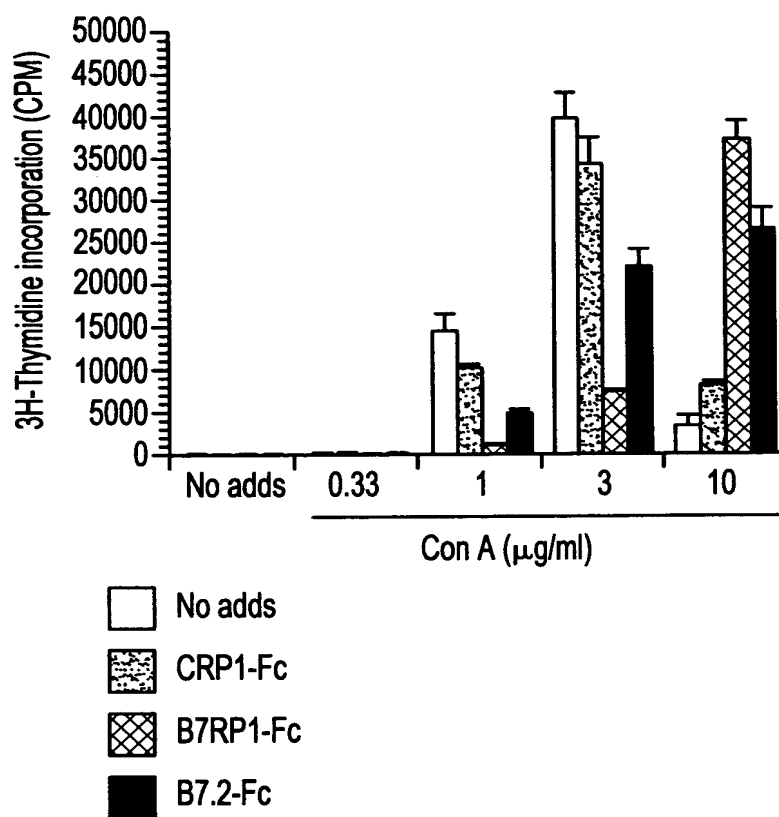


FIG. 9





PROCESSED BY
O.G. FIG.
SUBCLASS
DRAFTSMAN

FIG. 10A

Lymph node-control#10

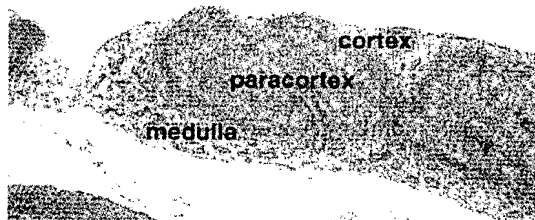


FIG. 10B

LN-WX11#40

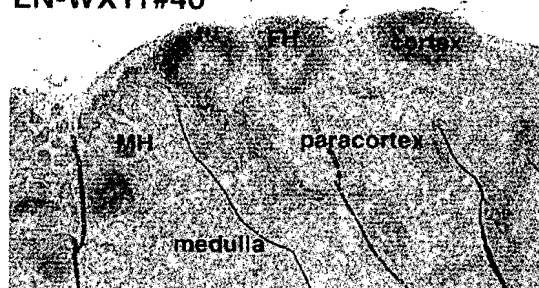


FIG. 10C

LN closeup-control#10

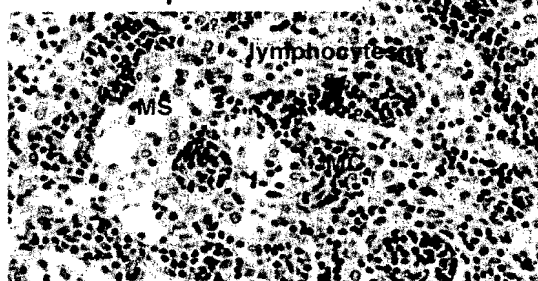


FIG. 10D

LN closeup-WX11#40

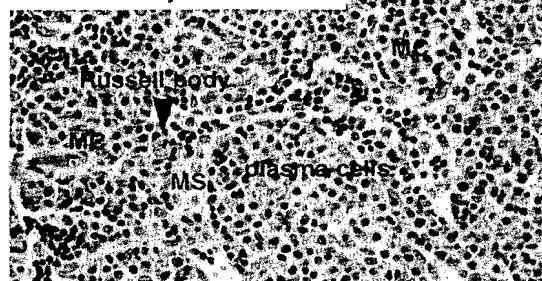


FIG. 10E

Spleen-control#10



FIG. 10F

Spleen-WX11#6



FIG. 10G

Ileum-control#25

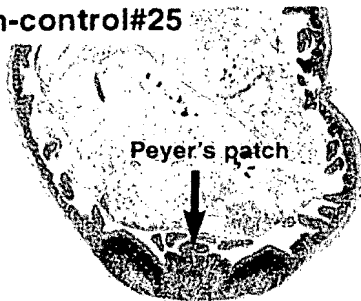


FIG. 10H

Ileum-WX11#32

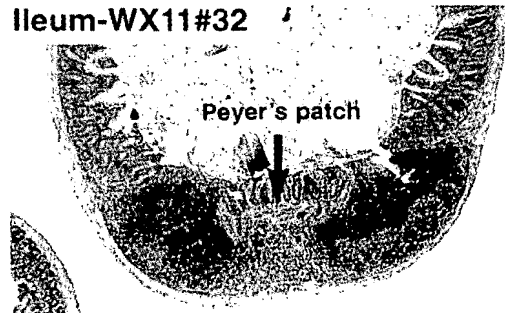
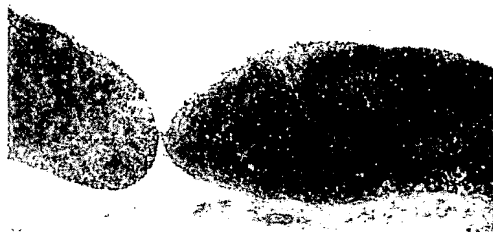




FIG. 11A



Control#5-H&E

FIG. 11B



WX11#33

FIG. 11C



Control-B220 (B cells)

FIG. 11D



WX11-B220

FIG. 11E



Control-CD3 (T cells)

FIG. 11F



WX11-CD3



FIGURE 12A.1

GCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCTGGGTCGACCCACGCGTCCGCCCACGCG -138
TCCGCGGGAGCGCAGTTAGAGCCGATCTCCCGCGCCCCGAGGTTGCTCCTCTCCGAGGTCTC -76
CCGCGGCCCCAAGTTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGTCTCCGCGGCCCCGAGGT -14
CTCCGCCCCGACC -1

ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC 45
M R L G S P G L L F L L F S S
5 10 15

CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC 90
L R A *D *T *Q *E K *E V R A *M V G
20 25 30

AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT 135
S D V E L S C A C P E G S R F
35 40 45

GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA 180
D L N D V Y V Y W Q T S E S K
50 55 60

ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC 225
T V V T Y H I P Q N S S L E N
65 70 75

GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC 270
V D S R Y R N R A L M S P A G
80 85 90

ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC 315
M L R G D F S L R L F N V T P
95 100 105

CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG 360
Q D E Q K F H C L V L S Q S L
110 115 120

GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA 405
G F Q E V L S V E V T L H V A
125 130 135

GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC 450
A N F S V P V V S A P H S P S
140 145 150

CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC 495
Q D E L T F T C T S I N G Y P
155 160 165

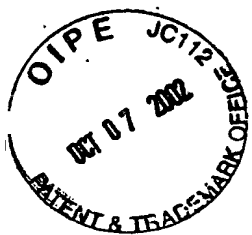
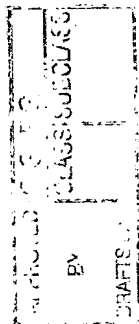


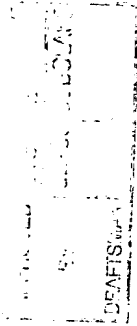
FIGURE 12A.2



AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG	540
R P N V Y W I N K T D N S L L	
170 175 180	
GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC	585
D Q A L Q N D T V F L N M R G	
185 190 195	
TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC	630
L Y D V V S V L R I A R T P S	
200 205 210	
GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC	675
V N I G C C I E N V L L Q Q N	
215 220 225	
CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC	720
L T V G S Q T G N D I G E R D	
230 235 240	
AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC	765
K I T E N P V S T G E K N A A	
245 250 255	
ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG	810
T W S I L A V L C L L V V V A	
260 265 270	
GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC	855
V A I G W V C R D R C L Q H S	
275 280 285	
TAT GCA GGT GCC TGG GCT GTG AGT CCG GAG ACA GAG CTC ACT GGC	900
Y A G A W A V S P E T E L T G	
300	
CAC GTT TGA	909
H V STOP	
302	
CCGGAGCTCACCGCCAGAGCGTGGACAGGGCTTCCGTGAGACGCCACCGTGAGAGGCCAGG	971
TGGCAGCTTGAGCATGGACTCCCAGACTGCAGGGGAGCACTTGGGGCAGCCCCAGGAAGGAC	1033
CACTGCTGGATCCCAGGGAGAACCTGCTGGCGTTGGCTGTGATCCTGGAATGAGGCCCTTTC	1095



FIGURE 12B



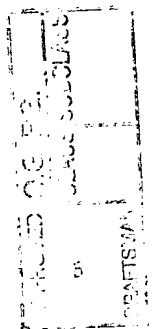
human	MRLGSP----	-----G	L-LF-LLFSS	LRADTQEKEV	25	
mouse	MQLKPCPCFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLLSS	LCAASAETEV	50
Consensus	M.L..P....G	L.LF.LL.SS	L.A...E.EV	50	
human	RAMVGSDEL	SCACPEGSRF	DLNDVYVYWQ	TSESKTVVTY	HIPQNSSLN	75
mouse	GAMVGSNVVL	SCIDPHRRHF	NLSGLYVYWQ	IENPEVSVTY	YLPYKSPGIN	100
Consensus	.AMVGS.V.L	SC..P....F	.L...YVYWQVTY	..P..S...N	100
human	VDSRYRNRAL	MSPAGMLRGD	FSLRLFNVTP	QDEQKFHCLV	LSQ-SLGFQE	124
mouse	VDSSYKNRGH	LSLDSMKQGN	FSLYLKNVTP	QDTQEFTCRV	FMNTATELVK	150
Consensus	VDS.Y.NR..	.S...M..G.	FSL.L.NVTP	QD.Q.F.C.V	150
human	VLSVEVTLHV	AANFSVPVVS	APHSPSQ-DE	LTFTCTSING	YPRPNVYWIN	173
mouse	ILEEVVRLRV	AANFSTPVIS	TSDSSNPGQE	RTYTCMSKNG	YPEPNLYWIN	200
Consensus	.L...V.L.V	AANFS.PV.S	...S.....E	.T.TC.S.NG	YP.PN.YWIN	200
human	KTDNSLLDQA	LQNDTVFLNM	RGLYDVVSVL	RIARTPSVNI	GCCIENVLLQ	223
mouse	TTDNSLIDTA	LQNNTVYLNK	LGLYDVISTL	RLPWTSRGDV	LCCVENVALH	250
Consensus	.TDNSL.D.A	LQN.TV.LN.	.GLYDV.S.L	R...T.....	.CC.ENV.L.	250
human	QNLTVGSQTG	NDIGERDKIT	ENPVSTGEKN	AATWSILAVL	CLLVVVAVAI	273
mouse	QNITSISQAE	SFTGNNTKNP	QETHNNELKV	LV--PVLAVL	AAAAFVSFII	298
Consensus	QN.T..SQ..	...G...K..K.LAVLV...I	300
human	GWVCRDRCLQ	HSYAGAWAVS	PETELTGHV			302
mouse	YR--RTR-PH	RSYTGPKTVQ	LE--LTDHA			322
ConsensusR.R...	.SY.G...V.	.E..LT.H.			329

FIGURE 13A.1

AACAAATTTACACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCTAATACGA															-111	
CTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTC															-56	
GACCCACGCGTCCGTGAACACTGAACGCGAGGACTGTTAAGTGTCTTCTGGCAAAC															-1	
ATG	AAG	TCA	GGC	CTC	TGG	TAT	TTC	TTT	CTC	TTC	TGC	TTG	CGC	ATT	45	
M	K	S	G	L	W	Y	F	F	L	F	C	L	R	I		
				5						10					15	
AAA	GTT	TTA	ACA	GGA	GAA	ATC	AAT	GGT	TCT	GCC	AAT	TAT	GAG	ATG	90	
K	V	L	T	*G	*E	I	N	G	S	A	N	Y	E	M		
				20						25					30	
TTT	ATA	TTT	CAC	AAC	GGA	GGT	GTA	CAA	ATT	TTA	TGC	AAA	TAT	CCT	135	
F	I	F	H	N	G	G	V	Q	I	L	C	K	Y	P		
				35						40					45	
GAC	ATT	GTC	CAG	CAA	TTT	AAA	ATG	CAG	TTG	CTG	AAA	GGG	GGG	CAA	180	
D	I	V	Q	Q	F	K	M	Q	L	L	K	G	G	Q		
				50						55					60	
ATA	CTC	TGC	GAT	CTC	ACT	AAG	ACA	AAA	GGA	AGT	GGA	AAC	ACA	GTG	225	
I	L	C	D	L	T	K	T	K	G	S	G	N	T	V		
				65						70					75	
TCC	ATT	AAG	AGT	CTG	AAA	TTC	TGC	CAT	TCT	CAG	TTA	TCC	AAC	AAC	270	
S	I	K	S	L	K	F	C	H	S	Q	L	S	N	N		
				80						85					90	
AGT	GTC	TCT	TTT	TTT	CTA	TAC	AAC	TTG	GAC	CAT	TCT	CAT	GCC	AAC	315	
S	V	S	F	F	L	Y	N	L	D	H	S	H	A	N		
				95						100					105	
TAT	TAC	TTC	TGC	AAC	CTA	TCA	ATT	TTT	GAT	CCT	CCT	CCT	TTT	AAA	360	
Y	Y	F	C	N	L	S	I	F	D	P	P	P	F	K		
				110						115					120	
GTA	ACT	CTT	ACA	GGA	GGA	TAT	TTG	CAT	ATT	TAT	GAA	TCA	CAA	CTT	405	
V	T	L	T	G	G	Y	L	H	I	Y	E	S	Q	L		
				125						130					135	
TGT	TGC	CAG	CTG	AAG	TTC	TGG	TTA	CCC	ATA	GGA	TGT	GCA	GCC	TTT	450	
C	C	Q	L	K	F	W	L	P	I	G	C	A	A	F		
				140						145					150	
GTT	GTA	GTC	TGC	ATT	TTG	GGA	TGC	ATA	CTT	ATT	TGT	TGG	CTT	ACA	495	
V	V	V	C	I	L	G	C	I	L	I	C	W	L	T		
				155						160					165	



FIGURE 13A.2



AAA AAG AAG TAT TCA TCC AGT GTG CAC GAC CCT AAC GGT GAA TAC	540
K K K Y S S S V H D P N G E Y	
170 175 180	
ATG TTC ATG AGA GCA GTG AAC ACA GCC AAA AAA TCT AGA CTC ACA	585
M F M R A V N T A K K S R L T	
185 190 195	
GAT GTG ACC CTA TAA	600
D V T L STOP	
199	
TATGGAACCTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCCTCAACTTGA	655
AGTGCAAGATTCTCTTATTTCCGGGACCACGGAGAGTCTGACTTAACTACATACA	710
TCTTCTGCTGGTGTTTTGTTCAATCTGGAAGAATGACTGTATCAGTCAATGGGGA	765
TTTTAACAGACTGCCTTGCTACTGCCGAGTCCTCTCAAAACAAACACCCCTCTTGC	820
AACCAGCTTTGGAGAAAAGCCCAGCTCCTGTGTGCTCACTGGGAGTGGAATCCCTG	875
TCTCCACATCTGCTCCTAGCAGTGCATCAGCCAGTAAACAAACACATTTACAAG	930
AAAAATGTTTTAAAGATGCCAGGGGTACTGAATCTGCAAAGCAAATGAGCAGCCA	985
AGGACCAGCATCTGTCCGCATTTCACTATCATACTACCTCTTCTTTCTGTAGGGA	1040
TGAGAATTCTCTTTTAATCAGTCAAGGGAGATGCTTCAAAGCTGGAGCTATTTT	1095
ATTTCTGAGATGTTGATGTGAACGTACATTAGTACATACTCAGTACTCTCCTTC	1150
AATTGCTGAACCCAGTTGACCATTTTACCAAGACTTTAGATGCTTTCTTGTGCC	1205

FIGURE 13B

hCRP1	MKSGWLWYFFLFCLRIKVLGTGEINGSANYEMFIFHNGGVQILCKYPDIVQQ	50
mCRP1	MKPYFCRVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQQ	50
hCRP1	FKMQLLKGGQILCDLTCTKKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNLD	100
mCRP1	LKMRLFREREVLCELTCTKKGSGNAVSINKPMLCLYHLSNNSVSFFLNND	100
hCRP1	HSHANYFNCNLSIFDPPPFKV.TLTGGYLHIYESQLCCQLKFWLPVIGCAA	149
mCRP1	SSQGSYYFCSLSIFDPPPFQERNLGGYLHIYESQLCCQLKLWLPVIGCAA	150
hCRP1	FVVVCILGCILICWLTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL	199
mCRP1	FVVVLLFGCILIIFWSKKKYGSSVHDPNSEYMFMAVNTNKKSLAGVTS	200

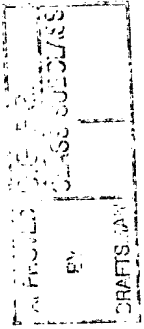


FIG. 14A

CD44

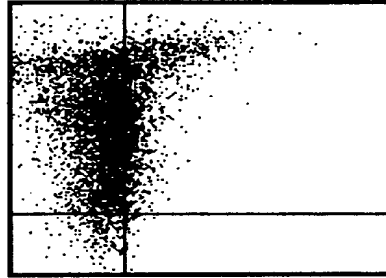


FIG. 14B

CD45RB

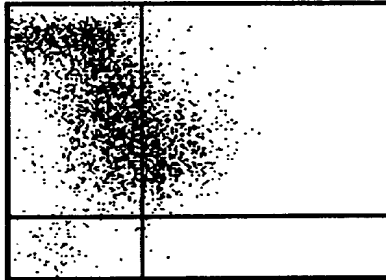


FIG. 14C

CD69



CRP-1
expression

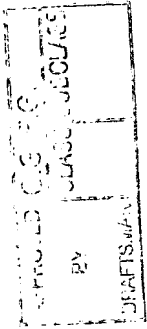


FIG. 15A

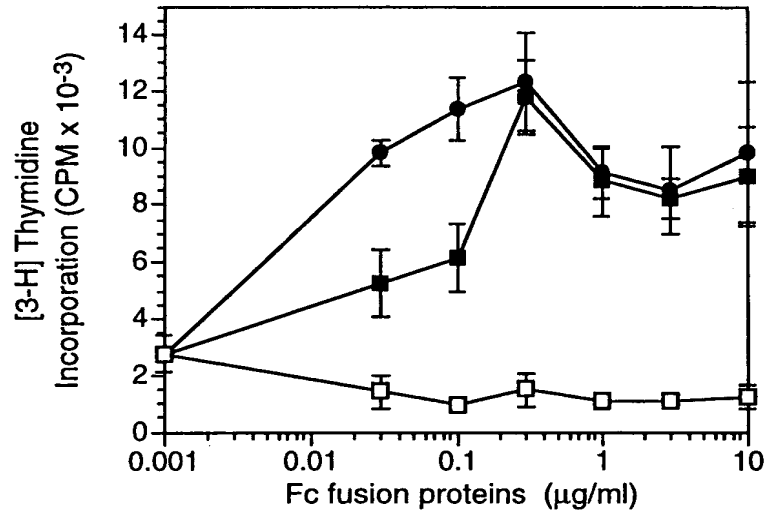
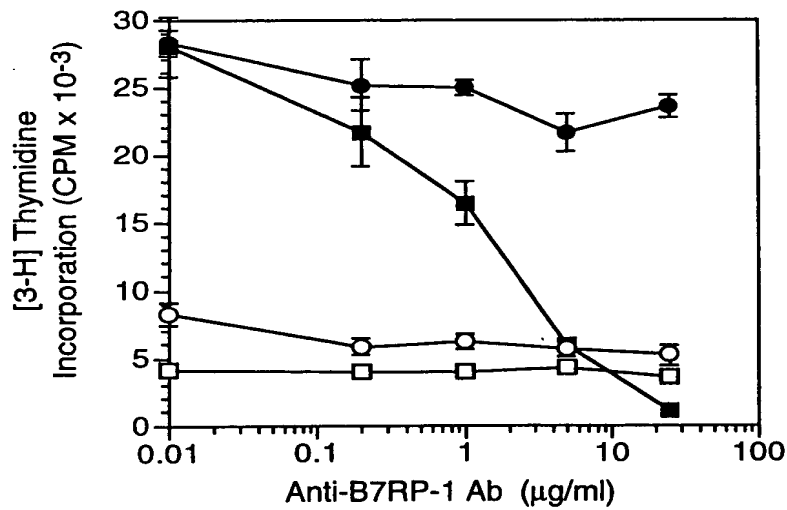


FIG. 15B



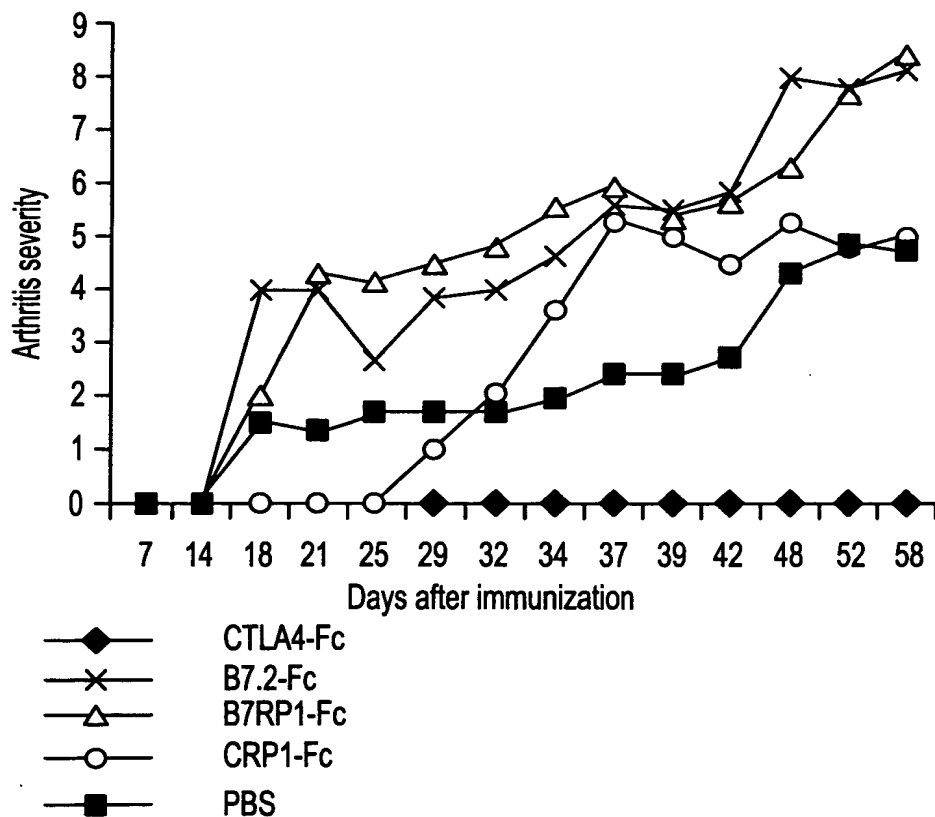
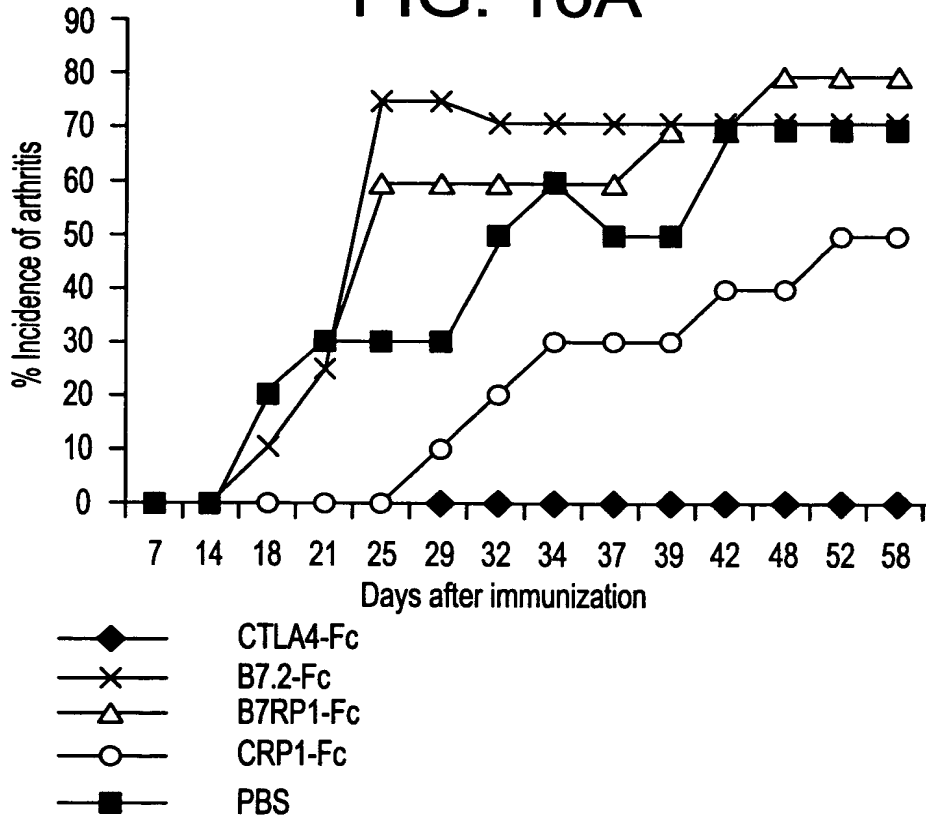
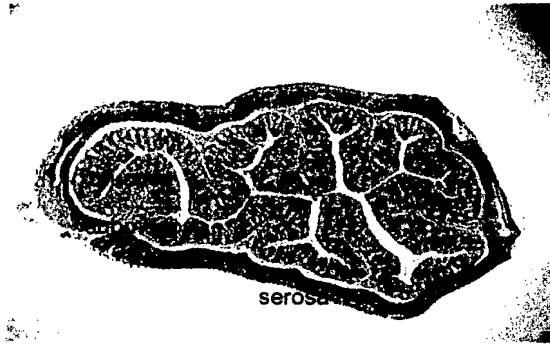


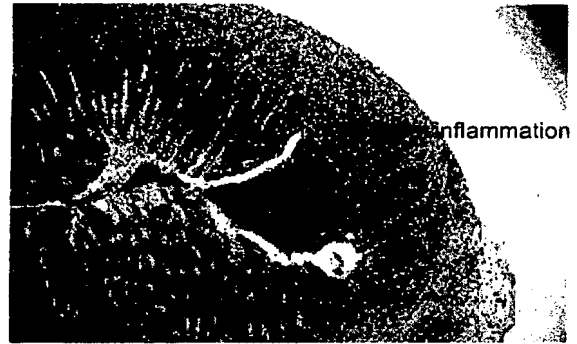


FIG. 17A



Control mouse#53F: Prox. colon 40X

FIG. 17B



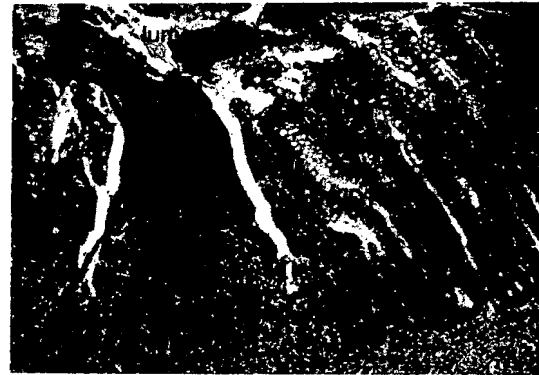
Mouse#111F: Prox. colon 40X

FIG. 17C



Mouse#111F: Prox. colon 20X

FIG. 17D



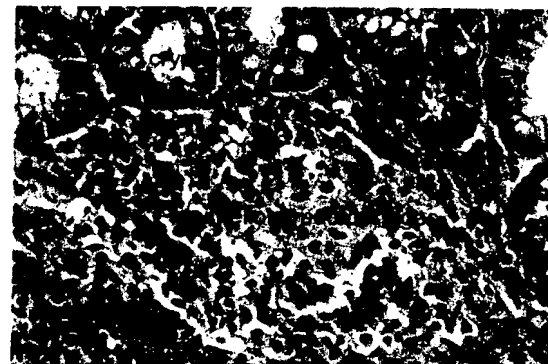
Mouse#111F: closeup of mucosa 100X

FIG. 17E



Mouse#112F: Giant cell, submucosa

FIG. 17F



Mouse#112F: epithelioid macrophages

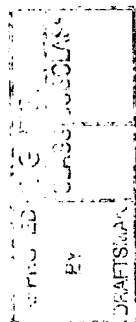
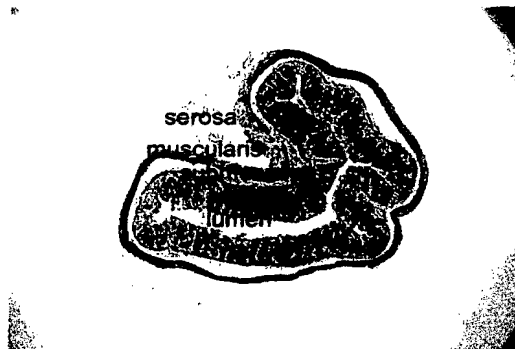
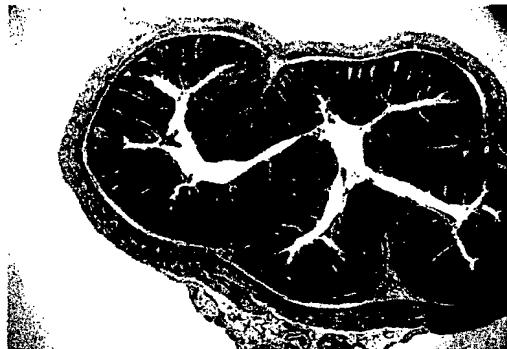


FIG. 18A



Control mouse#53F: Distal colon, 40X

FIG. 18B



Mouse#111F: Distal colitis, 40X

FIG. 18C



Mouse#55M: Distal colitis, 40X

FIG. 18D



Mouse#112F: Distal colon, 40X

FIG. 18E



Mouse#112: CD3+ T-cells, 40X

FIG. 18F



Mouse#112: closeup, 100X

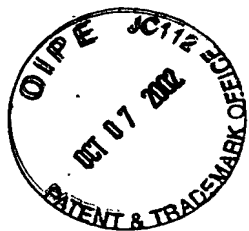


FIG. 19A



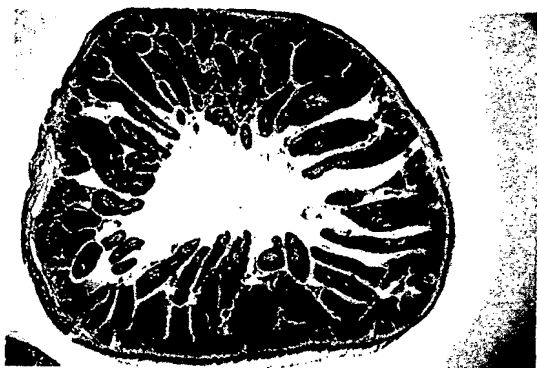
Control mouse#53F: duodenum, 40X

FIG. 19B



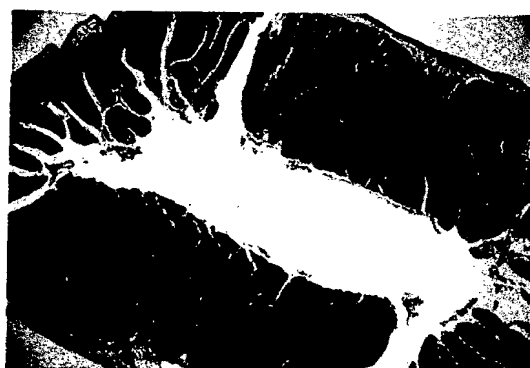
Mouse#51F: duodenum, 40X

FIG. 19C



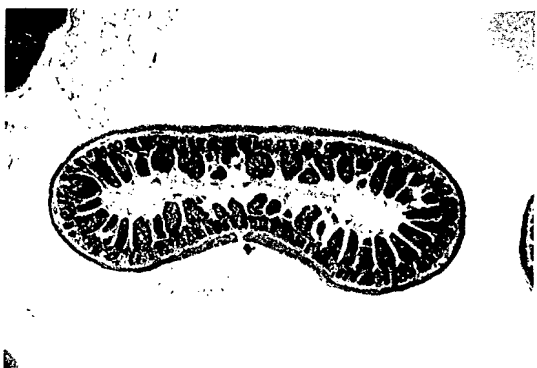
Control mouse#53F: jejunum, 40X

FIG. 19D



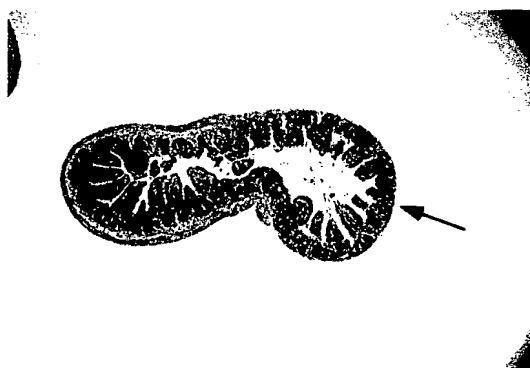
Mouse#51F: jejunal hyperplasia, 40X

FIG. 19E



Mouse#53F: ileum, 40X

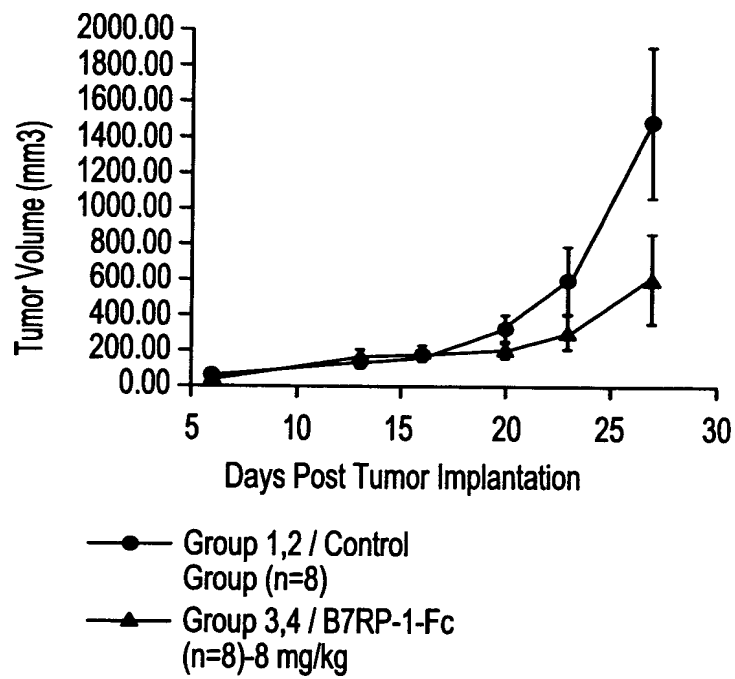
FIG. 19F



Mouse#231M: ileal atrophy, 40X



FIG. 20



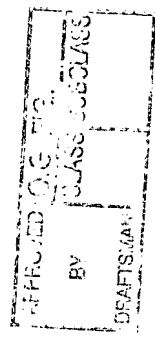
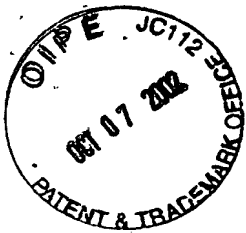


FIG. 21A

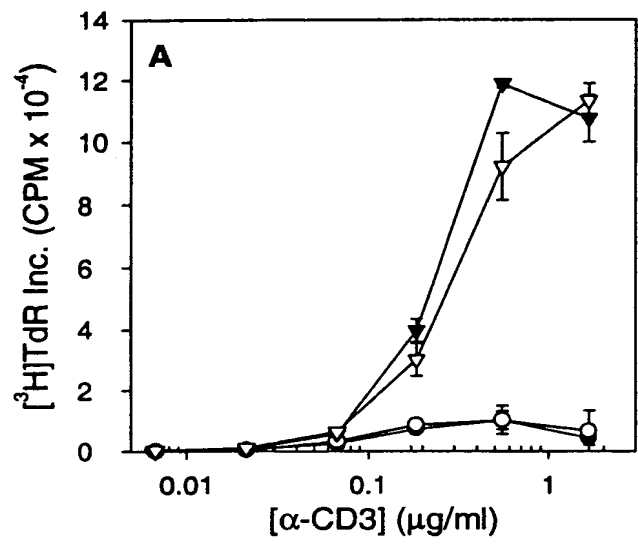


FIG. 21B

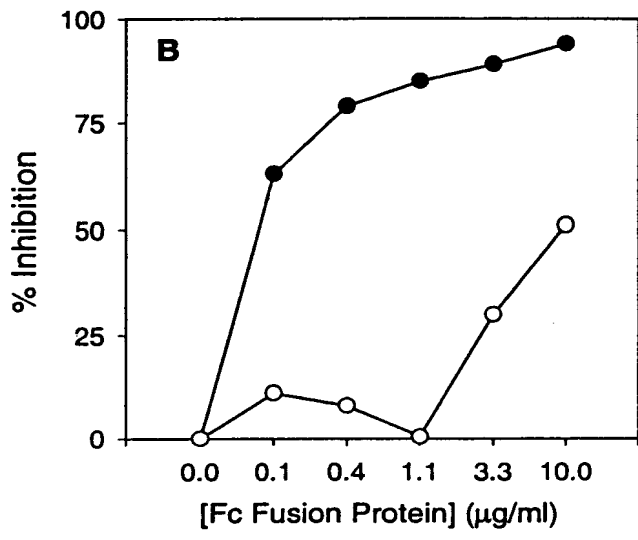


FIG. 21C

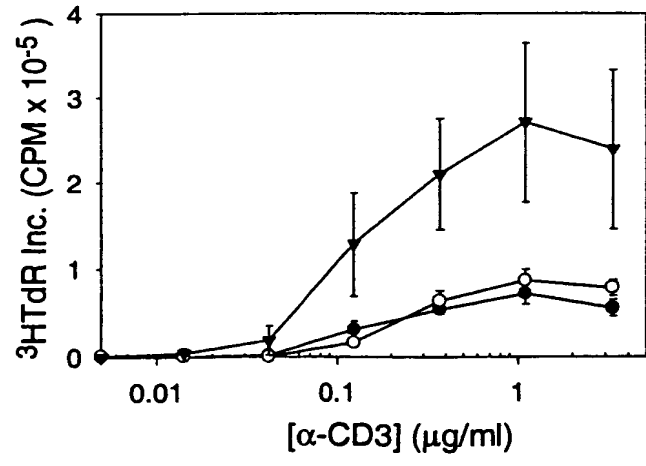




FIG. 21D

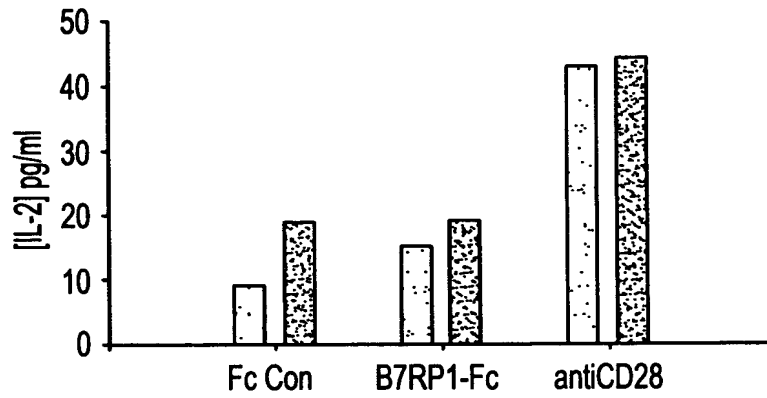


FIG. 21E

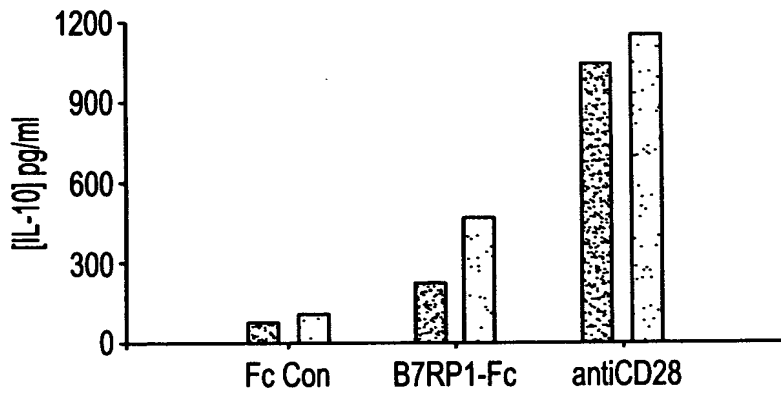


FIG. 21F

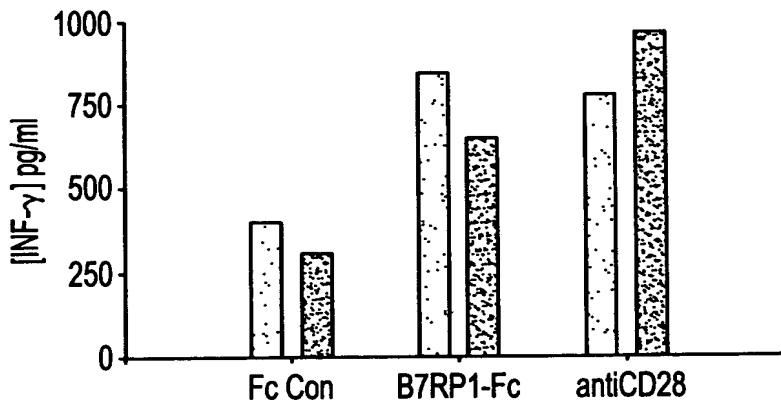




FIG. 22

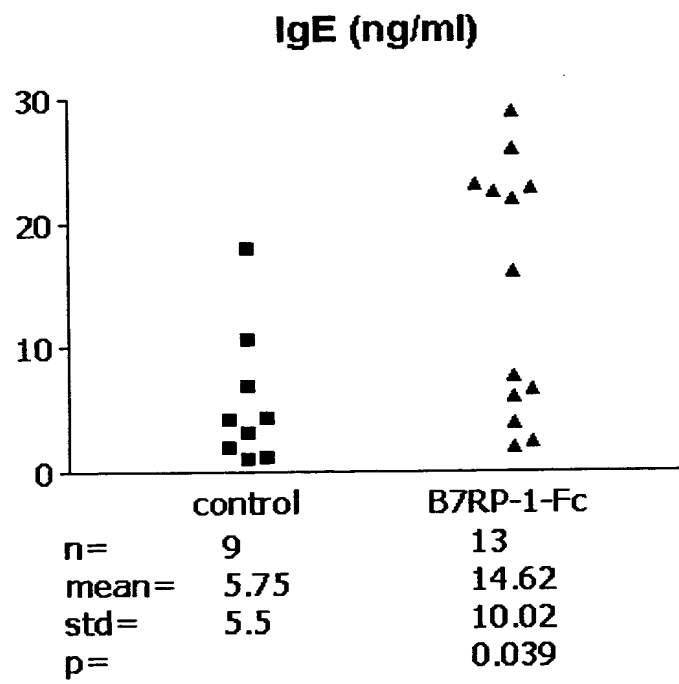




FIG. 23

■ B7RP-1-Fc ▲ B7.2-Fc
◆ B7RP-1-Fc+B7.2-Fc ○ Fc

